AMENDMENTS TO THE CLAIMS UNDER REVISED 37 C.F.R. § 1.121

Please amend the claims as follows:

1. (Currently Amended) An isolated nucleic acid molecule comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 1;

(b) of the DNA insert in ATCC Deposit No. PTA-1423;

(c) encoding a polypeptide as set forth in SEQ ID NO: 2;

(d) that hybridizes to the complement of the nucleotide sequence of any of (a) – (c) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences~~under at least moderately stringent conditions to the complement of the nucleotide sequence of any of (a) – (c)~~; or

(e) that is complementary to the nucleotide sequence of any of (a) - (d).

2. (Currently Amended) An isolated nucleic acid molecule comprising:

(a) a region of the nucleotide sequence of SEQ ID NO: 1, or the DNA insert in ATCC Deposit No. PTA-1423, encoding a polypeptide fragment of at least 25 amino acid residues~~, wherein the polypeptide fragment has an activity of the polypeptide set forth in SEQ ID NO: 2, or is antigenic~~;

(b) a region of the nucleotide sequence of SEQ ID NO: 1, or the DNA insert in ATCC Deposit No. PTA-1423, comprising a fragment of at least 16 nucleotides;

(c) a nucleotide sequence that hybridizes to the complement of the nucleotide sequence of either (a) or (b) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences~~under at least moderately stringent conditions to the complement of the nucleotide sequence of either (a) or (b)~~; or

(d) a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - (c).

3. (Currently Amended) An isolated nucleic acid molecule comprising:

(a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 70 percent identical to ~~has an activity of~~ the polypeptide set forth in SEQ ID NO: 2;

(b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 25 amino acid residues~~has an activity of the polypeptide set forth in SEQ ID NO: 2~~;

(c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein the encoded polypeptide is at least 70 percent identical to ~~has an activity of~~ the polypeptide set forth in SEQ ID NO: 2 and comprises at least 25 amino acid residues;

(d) a region of the nucleotide sequence of any of (a) - (c) comprising a fragment of at least 16 nucleotides;

(e) a nucleotide sequence that hybridizes to the complement of the nucleotide sequence of either (a) or (b) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences~~under at least moderately stringent conditions to the complement of the nucleotide sequence of any of (a) - (d)~~; or

(f) a nucleotide sequence that is complementary to any of (a) - (e).

4. (Original) A vector comprising the nucleic acid molecule of any of Claims 1, 2, or 3.

5. (Original) A host cell comprising the vector of Claim 4.

6. (Original) The host cell of Claim 5 that is a eukaryotic cell.

7. (Original) The host cell of Claim 5 that is a prokaryotic cell.

8. (Original) A process of producing an IL-1ra-R polypeptide comprising culturing the host cell of Claim 5 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture.

9. (Cancelled)

10. (Previously amended) The process of Claim 8, wherein the nucleic acid molecule comprises promoter DNA other than native IL-1ra-R promoter DNA operatively linked to a nucleic acid molecule encoding an IL-1ra-R polypeptide.

11. (Currently amended) The isolated nucleic acid molecule according to Claim ~~2~~3, wherein the percent identity is determined using a computer program that is GAP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, or the Smith-Waterman algorithm.

12-41. (Cancelled)

42. (Original) A composition comprising a nucleic acid molecule of any of Claims 1, 2, or 3 and a pharmaceutically acceptable formulation agent.

43. (Original) The composition of Claim 42, wherein said nucleic acid molecule is contained in a viral vector.

44. (Original) A viral vector comprising a nucleic acid molecule of any of Claims 1, 2, or 3.

45. (Previously amended) A nucleic acid molecule encoding a fusion polypeptide comprising the nucleic acid molecule of any of Claims 1, 2, or 3 fused to DNA encoding a heterologous amino acid sequence.

46. (Currently amended) The nucleic acid molecule of Claim 45, wherein the DNA encoding the heterologous amino acid sequence encodes an IgG constant domain ~~or biologically active fragment thereof~~.

47-56. (Cancelled)

57. (New) An isolated nucleic acid molecule comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 1;

(b) of the DNA insert in ATCC Deposit No. PTA-1423;

(c) encoding a polypeptide as set forth in SEQ ID NO: 2; or

(d) that is complementary to the nucleotide sequence of any of (a) - (c).